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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/090,672A**

DATE: 01/05/2000  
TIME: 04:16:25

INPUT SET: S34368.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply

Corrected Diskette Needed

## SEQUENCE LISTING

```

1
2
3 (1) General Information:
4   (i) APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
5       Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
6       Shigemasa; Takei, Masami
7   (ii) TITLE OF INVENTION: IgA Nephropathy-Related Genes
8   (iii) NUMBER OF SEQUENCES: 111
9   (iv) CORRESPONDENCE ADDRESS:
10    (A) ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
11    (B) STREET: 30 Rockefeller Plaza
12    (C) CITY: New York
13    (D) STATE: New York
14    (E) ZIP: 10112-3801
15   (v) COMPUTER READABLE FORM:
16    (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
17    (B) COMPUTER: Compac PC
18    (C) OPERATING SYSTEM: Windows 95
19    (D) SOFTWARE: WordPerfect 8.0
20   (vi) CURRENT APPLICATION DATA:
21    (A) APPLICATION NUMBER: 09/090,672
22    (B) FILING DATE: 04-JUNE-1998
23    (C) CLASSIFICATION: 435
24   (vii) PRIOR APPLICATION DATA:
25    (A) APPLICATION NUMBER: PCT/JP97/04468
26    (B) FILING DATE: 05-DEC-1997
27    (A) APPLICATION NUMBER: JP-8-325763
28    (B) FILING DATE: 05-DEC-1996
29   (viii) ATTORNEY/AGENT INFORMATION:
30    (A) NAME: Perry, Lawrence S.
31    (B) REGISTRATION NUMBER: 31865
32    (C) REFERENCE/DOCKET NUMBER: 766.21
33   (ix) TELECOMMUNICATION INFORMATION:
34    (A) TELEPHONE: (212) 218-2100
35    (B) TELEFAX: (212) 218-2200
36

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**ERRORED SEQUENCES FOLLOW:**

```

545   (2) INFORMATION FOR SEQ ID NO:8:
546     (i) SEQUENCE CHARACTERISTICS:
--> 547      (A) 278 base pairs

```



LENGTH:

*add other MANDATORY heading*

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TIME: 04:16:26

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548 (B) TYPE: nucleic acid  
549 (C) STRANDEDNESS: double  
550 (D) TOPOLOGY: linear  
551 (ii) MOLECULE TYPE: cDNA  
552 (vi) ORIGINAL SOURCE:  
553 (A) ORGANISM: human  
554 (G) CELL TYPE: leukocyte  
555 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
556 GAAGGAGAAAT ATGAAGAGGT TAGAAAAGNT CNGGNNTCTG TTGGTGAAAT GAAGGATGAA 60  
557 GGGGAAGAGA CATTAAATTAA TCCTGTACT ACCATTGACT TGTCTCACCT TCAACCCCAA 120  
558 AGGTCCATCC AGAAATTGGC TTCAAAAGAG GAATCTTCTA ATTCTAGTGA CAGTAAATCA 180  
559 CAGAGCCCGGA GACATTTGTC AGCCAAGGAA AGAAGGGAAA TGAAAAAGAA AAAACTTCCA 240  
560 AGTGACTCAG GAGATTAGA AGCGTTAGAG GGAAAGGA 278  
561

1044 (2) INFORMATION FOR SEQ ID NO:36:  
1045 (i) SEQUENCE CHARACTERISTICS:  
1046 (A) LENGTH: 133 amino acids 132 listed  
1047 (B) SEQUENCE TYPE: amino acid  
1048 (D) TOPOLOGY: linear + delete SEQUENCE - just use TYPE  
1049 (ii) MOLECULE TYPE: protein  
1050 (vi) ORIGINAL SOURCE:  
1051 (A) ORGANISM: human  
1052 (G) CELL TYPE: leukocyte  
1053 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:  
1054 Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr  
1055 1 5 10 15Pro Thr Ala  
1056 Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser 20 25 30 Insert band return  
1057 20 25 30 here  
1058 Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser  
1059 35 40 45  
1060 Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro  
1061 50 55 60  
1062 Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys  
1063 65 70 75 80  
1064 Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu  
1065 85 90 95  
1066 Ser Leu Glu Pro Ala Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys  
1067 100 105 110  
1068 Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe  
1069 115 120 125  
1070 Thr Arg Thr Asp Ile  
1071 130  
1072

1102 (2) INFORMATION FOR SEQ ID NO:38:  
1103 (i) SEQUENCE CHARACTERISTICS:  
--> 1104 (A) LENGTH: 128 amino acids  
--> 1105 *delete* (B) ~~SEQUENCE~~ TYPE: amino acid  
1106 (D) TOPOLOGY: linear  
1107 (ii) MOLECULE TYPE: protein  
1108 (vi) ORIGINAL SOURCE:  
1109 (A) ORGANISM: human

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1110      (G) CELL TYPE: leukocyte
1111      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
1112      Met Asp Ala Val Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly
1113          1           5           10           15
1114      Glu Lys Leu Leu Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg
1115          20          25           30
1116      Asp Ser Glu Ser Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His
1117          35          40           45
1118      Gly Tyr Ile Tyr Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp
1119          50          55           60
1120      Ser Ala Glu Thr Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile
1121          65          70           75           80
1122      Lys Asn Leu Ile Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile
1123          85          90           95
1124      Pro Leu Gln Tyr Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln
1125          100         105           110
1126      Gly Thr Thr Gly Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro
1127          115         120           125

```

add

1129 (2) INFORMATION FOR SEQ ID NO:39:  
 --> 1130 (A) LENGTH: 305 base pairs  
 --> 1131 (B) TYPE: nucleic acid  
 --> 1132 (C) STRANDEDNESS: double  
 --> 1133 (D) TOPOLOGY: linear  
 --> 1134 (E) MOLECULE TYPE: cDNA  
 1135 (F) ORIGINAL SOURCE:  
 1136 (A) ORGANISM: human  
 1137 (G) CELL TYPE: leukocyte  
 --> 1138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:  
 --> 1139 TCATGAAGTG AAGCCAAC TG TTTAGACTAG AATGTTATGA GATTAAACCC ACNNNNNNNTT 60  
 --> 1140 ATTCA TAGAC ATAAACCCCTC ATTTTAATTA GTGGATCTGG ATTTTTGTCA TATGTGGAAT 120  
 --> 1141 CATAATTCAA ACAAAATCAA CTAAGATGAT CCAAGTTCCA CACAAC TGCA CTTCAATATT 180  
 --> 1142 CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCACAAAGAT TCTGAGCTGT CGTAAAAGC 240  
 --> 1143 CTGGCTCGTG GTTTCTATT ATAGTGTACA CATGTTGGGT TATAATCACA AACCTGGAAC 300  
 --> 1144 TCTGT 305  
 1145

leads

1427 (2) INFORMATION FOR SEQ ID NO:66:  
--> 1428 (i) (1) SEQUENCE CHARACTERISTICS:  
--> 1429 (A) LENGTH: 22 base pairs  
--> 1430 ↑ (B) TYPE: nucleic acid  
--> 1431 use, (C) STRANDEDNESS: single  
--> 1432 not (D) TOPOLOGY: linear  
1433 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
--> 1434 (1) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:  
1435 GCGTGGAAATC AAATGGAGTG GC  
1436

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/090,672A**

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Line	Error	Original Text
23	Wrong Classification	(C) CLASSIFICATION: 435
532	Entered (155) and Calc. Seq. Length (278) differ	(A) LENGTH: 155 base pairs
547	Unknown or Misplaced Identifier	(A) 278 base pairs
1046	Entered (133) and Calc. Seq. Length (131) differ	(A) LENGTH: 133 amino acids
1047	Unknown or Misplaced Identifier	(B) SEQUENCE TYPE: amino acid
1104	Entered (128) and Calc. Seq. Length (0) differ	(A) LENGTH: 128 amino acids
1105	Unknown or Misplaced Identifier	(B) SEQUENCE TYPE: amino acid
1130	Unknown or Misplaced Identifier	(i) LENGTH: 305 base pairs
1131	Unknown or Misplaced Identifier	(A) TYPE: nucleic acid
1132	Unknown or Misplaced Identifier	(B) STRANDEDNESS: double
1133	Unknown or Misplaced Identifier	(C) TOPOLOGY: linear
1134	Unknown or Misplaced Identifier	(D) MOLECULE TYPE: cDNA
1138	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1140	Wrong Amino Acid Designator	ATTICATAGAC ATAAACCCTC ATTTTAATTAA GTGGA
1140	Wrong Amino Acid Designator	ATTICATAGAC ATAAACCCTC ATTTTAATTAA GTGGA
1140	Wrong Amino Acid Designator	ATTICATAGAC ATAAACCCTC ATTTTAATTAA GTGGA
1140	Wrong Amino Acid Designator	ATTICATAGAC ATAAACCCTC ATTTTAATTAA GTGGA
1140	Wrong Amino Acid Designator	ATTICATAGAC ATAAACCCTC ATTTTAATTAA GTGGA
1141	Wrong Amino Acid Designator	CATAATTAA ACAAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTAA ACAAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTAA ACAAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTAA ACAAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTAA ACAAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTAA ACAAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTAA ACAAAATCAA CTAAGATGAT CCAAG
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	TCTGT
1419	Entered (24) and Calc. Seq. Length (22) differ	(A) LENGTH: 24 base pairs
1428	Unknown or Misplaced Identifier	(1) SEQUENCE CHARACTERISTICS:
1429	Unknown or Misplaced Identifier	(A) LENGTH: 22 base pairs
1430	Unknown or Misplaced Identifier	(B) TYPE: nucleic acid

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Line	Error	Original Text
1431	Unknown or Misplaced Identifier	(C) STRANDEDNESS: single
1432	Unknown or Misplaced Identifier	(D) TOPOLOGY: linear
1434	Wrong Or Missing Strandedness Value	(xi)SEQUENCE DESCRIPTION: SEQ ID NO:66:
1434	Wrong or Missing Sequence Topology	(xi)SEQUENCE DESCRIPTION: SEQ ID NO:66: